

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 16, 2005, 16:16:11 ; Search time 9.04128 Seconds  
(without alignments)  
2330.584 Million cell updates/sec

Title: US-10-003-356-2

Perfect score: 1138

Sequence: 1 MFERRKQDEGPGIHEFLAF.....RVIASDKIQSKAVVKRIQHF 219

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	353	31.0	1078	2 A56715	calcium receptor (
2	353	31.0	1088	2 B56715	calcium receptor (
3	351	30.8	1079	2 I59362	calcium/polyvalent
4	349	30.7	1085	2 S40476	Ca(2+)-sensing rec
5	239.5	21.0	1218	2 S71376	glutamate receptor
6	234.5	20.6	879	2 JC7160	metabotropic gluta
7	227	19.9	1180	2 JC2132	metabotropic gluta
8	227	19.9	1212	2 JC2131	metabotropic gluta
9	225.5	19.8	908	2 I49142	metabotropic gluta
10	224.5	19.7	1171	2 A42916	metabotropic gluta
11	222.5	19.6	912	2 JH0563	metabotropic gluta
12	221.5	19.5	879	2 JH0562	metabotropic gluta
13	220.5	19.4	915	2 A49874	metabotropic gluta
14	217.5	19.1	858	2 JC7683	taste receptor T1R
15	215	18.9	1199	2 A41339	G protein-coupled
16	203.5	17.9	872	2 JH0561	metabotropic gluta
17	191	16.8	871	2 A46742	metabotropic gluta
18	177.5	15.6	1267	2 T21340	hypothetical prote
19	176	15.5	999	2 T27628	hypothetical prote
20	86.5	7.6	921	2 T51136	ionotropic glutama
21	86.5	7.6	923	2 F84732	probable ligand-ga
22	85.5	7.5	442	2 T33246	hypothetical prote
23	84.5	7.4	642	2 G64605	iron(II) transport
24	84	7.4	960	2 A71315	excinuclease ABC c
25	83.5	7.3	303	2 A64423	modification methy
26	82	7.2	294	2 S59774	probable membrane
27	81.5	7.2	172	2 H71112	hypothetical prote
28	81	7.1	500	2 C69428	hypothetical prote
29	81	7.1	960	2 JB0356	gamma-aminobutyric

30	80.5	7.1	458	1 NICLMB	nitrogenase (BC 1.
31	80	7.0	231	2 T49830	hypothetical prote
32	80	7.0	570	2 F70332	proline-trna synth
33	79.5	7.0	296	2 B53434	cell surface glyco
34	79.5	7.0	335	2 A53434	cell surface glyco
35	79.5	7.0	501	2 A69415	conserved hypothet
36	79.5	7.0	654	1 P4XRBB	minor inner core p
37	79.5	7.0	1240	1 DJBE21	DNA-directed DNA p
38	78.5	6.9	990	2 F88925	protein T22H9.3 (i
39	78	6.9	933	2 C96495	probable ligand-ga
40	78	6.9	940	2 A82329	excinuclease ABC c
41	77.5	6.8	642	2 D71909	ferrous iron trans
42	77.5	6.8	970	2 C84488	hypothetical prote
43	77	6.8	441	2 H97112	probable rRNA meth
44	76.5	6.7	294	2 T20338	hypothetical prote
45	76.5	6.7	306	2 F72606	probable methanol

ALIGNMENTS

RESULT 1

A56715  
Calcium receptor (clone phPCaR-4.0) - human  
C:Species: Homo sapiens (man)  
C>Date: 19-Oct-1995 #sequence revision 19-Oct-1995 #text\_change 01-Dec-2000  
C:Accession: A56715; S49341; A49419; B49419; C49419  
R:Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C.  
J. Biol. Chem. 270, 12919-12925 1995  
A:Title: Molecular cloning and functional expression of human parathyroid calcium recep  
A:Reference number: A56715; MUID:95279439; PMID:7759551  
A:Accession: A56715  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1078 <GAR>  
A:Cross-references: GB:U20759; NID:9683744; PIDN:AAA86503.1; PID:9683745  
R:Pearce, S.H.S.; Thakker, R.V.  
submitted to the EMBL Data Library, August 1994  
A:Reference number: S49341  
A:Accession: S49341  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-180, 'Q', 182-989, 'R', 991-1078 <PEA>  
A:Cross-references: EMBL:X81086  
R:Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi,  
Cell 75, 1297-1303, 1993  
A:Title: Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalciur  
A:Reference number: A49419; MUID:94094324; PMID:7916660  
A:Accession: A49419  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 178-192 <POL>  
A:Experimental source: family N  
A:Note: sequence inconsistent with nucleotide translation  
A:Note: sequence modified after extraction from NCBI backbone  
A:Note: 186-Arg mutation is associated with familial hypocalciuric hypercalcemia and ne  
A:Note: sequence extracted from NCBI backbone (NCBIN:142453)  
A:Accession: B49419  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 289-303 <PO2>  
A:Experimental source: family E  
A:Note: sequence modified after extraction from NCBI backbone  
A:Note: 298-Lys mutation is associated with familial hypocalciuric hypercalcemia and ne  
A:Note: sequence extracted from NCBI backbone (NCBIN:142455)  
A:Accession: C49419  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 788-802 <PO3>  
A:Experimental source: family J  
A:Note: sequence modified after extraction from NCBI backbone  
A:Note: 796-Trp mutation is associated with familial hypocalciuric hypercalcemia and ne  
A:Note: sequence extracted from NCBI backbone (NCBIN:142457)

C;Keywords: glycoprotein; receptor; transmembrane protein

Query Match 31.0%; Score 353; DB 2; Length 1078;  
 Best Local Similarity 37.1%; Pred. No. 7e-25; Mismatches 64; Indels 24; Gaps 5;  
 Matches 78; Conservative 44;  
 QY 18 LAFW--AELGSEAKEKEERTCLLKCVDNAENHSLVIGLFPIDSRTPANESI-LE 74  
 DB 11 LALTHTSAYGPDQRAQKGD-----IILGGLFPIHFGVAAKQDLKSR 54  
 QY 75 PASAKCEGFNFRFMKAMIMHKEINKRKDILPNITLGYQIFDTCFTISKSVEAVLVF 134  
 DB 55 PESVEICIRNFRGFWLQAMIFAIEEINSSPALLPNLTGRIEDTCNTVSKALEATLSF 114  
 QY 135 LTQGE---ENRNFNRSNGTAPPA--GIVGAGSFLSVPASRIILGLYLPQVGTSTCVIL 189  
 DB 115 VAQNKIDSLNLDLFCNCSEHIPSTIAVVGATSGVSTAVANLGLFIYIPQVSYASSRLL 174  
 QY 190 SDKYQPSYLRVIASDKIQSKAVVKRIQHF 219  
 DB 175 SNKNQKSLRTPINDEHQATAMADIIIEYF 204  
 RESULT 2  
 B56715  
 C;Species: Homo sapiens (man)  
 C;Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 21-Jul-2000  
 C;Accession: B56715  
 R;Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C.  
 J. Biol. Chem. 270, 12919-12925, 1995  
 A;Title: Molecular cloning and functional expression of human parathyroid calcium receptor  
 A;Reference number: A56715; MUID:95279439; PMID:7759551  
 A;Accession: B56715  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-1088 <GAR>  
 A;Cross-references: GB:U20760; NID:G683746; PIDN:AAA86504.1; PID:G683747  
 C;Keywords: glycoprotein; receptor; transmembrane protein

Query Match 31.0%; Score 353; DB 2; Length 1088;  
 Best Local Similarity 37.1%; Pred. No. 7e-25; Mismatches 64; Indels 24; Gaps 5;  
 Matches 78; Conservative 44;  
 QY 18 LAFW--AELGSEAKEKEERTCLLKCVDNAENHSLVIGLFPIDSRTPANESI-LE 74  
 DB 11 LALTHTSAYGPDQRAQKGD-----IILGGLFPIHFGVAAKQDLKSR 54  
 QY 75 PASAKCEGFNFRFMKAMIMHKEINKRKDILPNITLGYQIFDTCFTISKSVEAVLVF 134  
 DB 55 PESVEICIRNFRGFWLQAMIFAIEEINSSPALLPNLTGRIEDTCNTVSKALEATLSF 114  
 QY 135 LTQGE---ENRNFNRSNGTAPPA--GIVGAGSFLSVPASRIILGLYLPQVGTSTCVIL 189  
 DB 115 VAQNKIDSLNLDLFCNCSEHIPSTIAVVGATSGVSTAVANLGLFIYIPQVSYASSRLL 174  
 QY 190 SDKYQPSYLRVIASDKIQSKAVVKRIQHF 219  
 DB 175 SNKNQKSLRTPINDEHQATAMADIIIEYF 204  
 RESULT 3  
 I59362  
 calcium/polyvalent cation-sensing receptor precursor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C;Accession: I59362; A55594  
 R;Ruat, M.; Molliver, M.E.; Snowman, A.M.; Snyder, S.H.  
 Proc. Natl. Acad. Sci. U.S.A. 92, 3161-3165, 1995  
 A;Title: Calcium sensing receptor: molecular cloning in rat and localization to nerve terminal  
 A;Reference number: I59362; MUID:95241465; PMID:7724534  
 A;Accession: I59362  
 A;Status: translated from GB/EMBL/DBEY

A;Molecule type: mRNA  
 A;Residues: 1-1079 <RES>  
 A;Cross-references: UNIPROT:P48442; EMBL:U20289; NID:G790578; PIDN:AAC52195.1; PID:G790578  
 A;Experimental source: striatal  
 R;Riccardi, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.; Hebert, S.C.  
 Proc. Natl. Acad. Sci. U.S.A. 92, 131-135, 1995  
 A;Title: Cloning and functional expression of a rat kidney extracellular calcium/polyvalent cation-sensing receptor  
 A;Reference number: A55594; MUID:95116508; PMID:7816802  
 A;Accession: A55594  
 A;Molecule type: mRNA  
 A;Residues: 1-133, 'X', 135-1079 <RIC>  
 A;Cross-references: GB:U10354  
 A;Experimental source: kidney  
 C;Keywords: calcium; glycoprotein; phosphoprotein; transmembrane protein  
 F;1-20/Domain: signal sequence #status predicted <SIG>  
 F;187-212/Region: hydrophobic  
 F;613-635/Domain: transmembrane #status predicted <TM1>  
 F;650-670/Domain: transmembrane #status predicted <TM2>  
 F;683-700/Domain: transmembrane #status predicted <TM3>  
 F;725-744/Domain: transmembrane #status predicted <TM4>  
 F;770-790/Domain: transmembrane #status predicted <TM5>  
 F;806-828/Domain: transmembrane #status predicted <TM6>  
 F;841-860/Domain: transmembrane #status predicted <TM7>  
 F;90, 261, 287, 386, 468, 488, 594, 893, 1005/Binding site: carbohydrate (asn) (covalent) #status predicted  
 F;794/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
 F;899, 901/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted  
 Query Match 30.8%; Score 351; DB 2; Length 1079;  
 Best Local Similarity 36.7%; Pred. No. 1.1e-24;  
 Matches 77; Conservative 45; Mismatches 64; Indels 24; Gaps 5;  
 QY 18 LAFW--AELGSEAKEKEERTCLLKCVDNAENHSLVIGLFPIDSRTPANESI-LE 74  
 DB 11 LALAHSSAYGPDQRAQKGD-----IILGGLFPIHFGVAAKQDLKSR 54  
 QY 75 PASAKCEGFNFRFMKAMIMHKEINKRKDILPNITLGYQIFDTCFTISKSVEAVLVF 134  
 DB 55 PESVEICIRNFRGFWLQAMIFAIEEINSSPALLPNLTGRIEDTCNTVSKALEATLSF 114  
 QY 135 LTQGE---ENRNFNRSNGTAPPA--GIVGAGSFLSVPASRIILGLYLPQVGTSTCVIL 189  
 DB 115 VAQNKIDSLNLDLFCNCSEHIPSTIAVVGATSGVSTAVANLGLFIYIPQVSYASSRLL 174  
 QY 190 SDKYQPSYLRVIASDKIQSKAVVKRIQHF 219  
 DB 175 SNKNQKSLRTPINDEHQATAMADIIIEYF 204  
 RESULT 4  
 S40476  
 Ca(2+)-sensing receptor - bovine  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
 C;Accession: S40476  
 R;Brown, E.M.; Gamba, G.  
 Nature 366, 575-580, 1993  
 A;Title: Cloning and characterization of an extracellular Ca(2+)-sensing receptor from b  
 A;Reference number: S40476; MUID:9407182; PMID:8255296  
 A;Accession: S40476  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-1085 <BRO>  
 A;Cross-references: UNIPROT:P35384; GB:S67307; NID:G453108; PIDN:AAB29171.1; PID:G453109  
 Query Match 30.7%; Score 349; DB 2; Length 1085;  
 Best Local Similarity 42.2%; Pred. No. 1.7e-24;  
 Matches 73; Conservative 38; Mismatches 56; Indels 6; Gaps 3;  
 QY 53 IIVGLGLFPIHFGVAAKQDLKSR--LEPASAKCEGFNFRFMKAMIMHKEINKRKDILPNI 111  
 DB 33 IILGGLFPIHFGVAAKQDLKSR--LEPASAKCEGFNFRFMKAMIMHKEINKRKDILPNI 92  
 QY 112 TLGQIFDTCFTISKSVEAVLVFLTGQE---ENRNFNRSNGTAPPA--GIVGAGSFLSV 166

Db 93 TLGYRIEDTCNTVSKALEATLSVAQNKIDSLNLEDFNCSEHIPPETIAVVGATSGIST 152  
QY 167 PASRIIGLYLPQGVYTCVILSDKYQPPSYLRVIASDKIOSKAVVKRIQHF 219  
Db 153 AVANLLGLFYIPQVSYASSRLLSNKQPKSFLRTIPDNEHQATWADIIEIF 205

RESULT 5  
S71376  
glutamate receptor homolog - cherry salmon  
C:Species: Oncorhynchus masou (cherry salmon)  
C:Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 09-Jul-2004  
C:Accession: S71376  
R:Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.  
FEBS Lett. 392, 71-76, 1996  
A:Title: Cloning and characterization of a bifunctional metabotropic receptor activated by glutamate and ATP  
A:Reference number: S71376; PMID:96354880; PMID:8769318  
A:Accession: S71376  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-1218 <KUB>  
A:Cross-references: UNIPROT:Q90ZF3  
C:Keywords: glycoprotein; phosphoprotein  
F:603-625/Domain: transmembrane #status predicted <TM1>  
F:640-660/Domain: transmembrane #status predicted <TM2>  
F:672-690/Domain: transmembrane #status predicted <TM3>  
F:717-737/Domain: transmembrane #status predicted <TM4>  
F:761-782/Domain: transmembrane #status predicted <TM5>  
F:796-817/Domain: transmembrane #status predicted <TM6>  
F:826-850/Domain: transmembrane #status predicted <TM7>  
F:104-233, 403, 525, 757/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:636, 699, 961/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
F:705/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
F:892/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predicted

Query Match 21.0%; Score 239.5; DB 2; Length 1218;  
Best Local Similarity 29.5%; Pred. No. 4.1e-14;  
Matches 56; Conservative 46; Mismatches 57; Indels 31; Gaps 6;

QY 53 LVIGGLFPIDSRTPANESILEPASAKC-----EGNFQFRPWKAMHMIKEINKRKDIL 108  
Db 51 IIGALFSVHHQ--PSTEQV--AERKCGEVREYGIQIR---VEAMFHTLDRINSNPILL 102  
QY 109 PNITLGYQIFDTCFTTSKSVAVLVLTG-----QEENR-----PNFRNFT 149  
Db 103 PNITLCEIRDSCHWSVALEQSIERFIRDSLSIRDDNDKGTSGROWCTEGHPPSQPAT 162  
QY 150 GAPAGIVGAGGFLSVPASRIILGLYLPQGVYTCVILSDKYQPPSYLRVIASDKIOS 209  
Db 163 KRPIAGVIGPGSSVAIQVQLQLFNIQIAYSATSIDLSDKTLFKYFLRVVPSDTLQA 222  
QY 210 KAVVKRIQHF 219  
Db 223 RAILEDIVKRY 232

RESULT 6  
JC7160  
metabotropic glutamate receptor subtype 3 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 04-Mar-2000 #sequence\_revision 04-Mar-2000 #text\_change 11-May-2000  
C:Accession: JC7160  
R:Minoshima, T.; Nakanishi, S.  
J. Biochem. 126, 889-896, 1999  
A:Title: Structural organization of the mouse metabotropic glutamate receptor subtype 3  
A:Reference number: JC7160; PMID:20012997; PMID:10544282  
A:Accession: JC7160  
A:Molecule type: DNA  
A:Residues: 1-879 <MIN>  
A:Cross-references: GB:AF170696  
C:Genetics:  
A:Gene: mGluR3

C:Superfamily: metabotropic glutamate receptor 4  
C:Keywords: differentiation; G protein-coupled receptor; receptor; transmembrane protein  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-879/Product: metabotropic glutamate receptor subtype 3 #status predicted <MAT>  
F:577-599/Domain: transmembrane #status predicted <TM1>  
F:614-634/Domain: transmembrane #status predicted <TM2>  
F:646-664/Domain: transmembrane #status predicted <TM3>  
F:689-709/Domain: transmembrane #status predicted <TM4>  
F:735-756/Domain: transmembrane #status predicted <TM5>  
F:770-791/Domain: transmembrane #status predicted <TM6>  
F:804-828/Domain: transmembrane #status predicted <TM7>

Query Match 20.6%; Score 234.5; DB 2; Length 879;  
Best Local Similarity 31.5%; Pred. No. 8.1e-14;  
Matches 57; Conservative 36; Mismatches 63; Indels 25; Gaps 5;

QY 53 LVIGGLFPIDSRTPANESILEPASAKC-----EGNFQFRPWKAMHMIKEINKRKDIL 111  
Db 39 LVIGGLFPINERKGTGTE-----CRGINEDRGIOLEALFAIDSEINKNDYLLPGV 89  
QY 112 TLGYQIFDTC-----FTISKSVEAVLVLTGQENRPNFRNSTCAPP-----AGIVG 158  
Db 90 KLGVLHLDTCSDTYALEQSLFVRSALTKVDE--AYMCPDGSVAIOENIPLLIAGVIG 147  
QY 159 AGGSFLSVPASRIILGLYLPQGVYTCVILSDKYQPPSYLRVIASDKIOSKAVVKRIQ 218  
Db 148 GSYSVSIQVANLLRFQIPQISYASTSAKLSKSRDYFARTVPPDFYQAKAMAILRY 207  
QY 219 F 219  
Db 208 F 208

RESULT 7  
JC2132  
metabotropic glutamate receptor 5 A - human  
C:Species: Homo sapiens (man)  
C:Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 05-Jan-1996  
C:Accession: JC2132  
R:Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.  
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994  
A:Title: Molecular cloning and the functional expression of two isoforms of human metabotropic glutamate receptor 5  
A:Reference number: JC2131; PMID:94197696; PMID:7908515  
A:Accession: JC2132  
A:Molecule type: mRNA  
A:Residues: 1-1180 <MIN>  
C:Comment: This protein is coupled to guanine nucleotide binding proteins.  
C:Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein  
F:580-604/Domain: transmembrane #status predicted <TM1>  
F:617-637/Domain: transmembrane #status predicted <TM2>  
F:644-664/Domain: transmembrane #status predicted <TM3>  
F:694-714/Domain: transmembrane #status predicted <TM4>  
F:738-759/Domain: transmembrane #status predicted <TM5>  
F:773-794/Domain: transmembrane #status predicted <TM6>  
F:803-827/Domain: transmembrane #status predicted <TM7>

Query Match 19.9%; Score 227; DB 2; Length 1180;  
Best Local Similarity 30.6%; Pred. No. 5.9e-13;  
Matches 56; Conservative 44; Mismatches 59; Indels 24; Gaps 7;

QY 53 LVIGGLFPIDSRTPANESILEPASAKC-----EGNFQFRPWKAMHMIKEINKRKDIL 108  
Db 35 IIGALFSVHHQ--PTVDKVHE---RKCQAVREYGIQIR---VEAMLTLEIRNSDPTLL 86  
QY 109 PNITLGYQIFDTCF-----TISKSVEAVLVLTGQENRPNFR---NSTGAPPA-----GI 156  
Db 87 PNITLCEIRDSCHWSVALEQSIERFIRDSLSISSEEEGLVRCVDSGSSFSKPKPIGV 146  
QY 157 VGAGSFLSVPASRIILGLYLPQGVYTCVILSDKYQPPSYLRVIASDKIOSKAVVKRI 216  
Db 147 ICGSSSVAIQVQLQLFNIQIAYSATSIDLSDKTLFKYFLRVVPSDAQARAWDIV 206  
QY 217 QHF 219

```

Db          207 KRY 209
:
:
:
RESULT 8
JC2131
metabotropic glutamate receptor 5 B - human
C:Species: Homo sapiens (man)
C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
C:Accession: JC2131
R;Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
A>Title: Molecular cloning and the functional expression of two isoforms of human metabo
A:Reference number: JC2131; MUID:94197696; PMID:7908515
A:Accession: JC2131
A:Molecule type: mRNA
A:Residues: 1-1212 <MIN>
C:Comment: This protein is coupled to guanine nucleotide binding proteins.
C:Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein
F;580-604/Domain: transmembrane #status predicted <TM1>
F;617-637/Domain: transmembrane #status predicted <TM2>
F;644-664/Domain: transmembrane #status predicted <TM3>
F;694-714/Domain: transmembrane #status predicted <TM4>
F;738-759/Domain: transmembrane #status predicted <TM5>
F;773-794/Domain: transmembrane #status predicted <TM6>
F;803-827/Domain: transmembrane #status predicted <TM7>
Query Match          19.9%; Score 227; DB 2; Length 1212;
Best Local Similarity 30.6%; Pred. No. 6.1e-13;
Matches 56; Conservative 44; Mismatches 59; Indels 24; Gaps 7;
QY 53 LVIGGLFPIDRTIPANESILEPASAKC-----EGFNQFRFRWKKAMHMIKEINKRKDIL 108
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 35 IIGALFVSHQ--PTVDKVHE---RKGAVREQYGIQR---VEAMLHTLERINSDPTLL 86
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 109 PNITLGYQIFDTCF-----TISKSEAVLVLTGQENRPNFR---NSTGAPPA-----GI 156
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 87 PNITLGCIRDSCHWSAVALRQSEIFRDSLSISEEGLVRCVDSGSSFRSKKPIVGV 146
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 157 VCAGGSFLSPASRLGLYLPOVGYTSTCVILSDKYQPPSYLRVLTASDKIQSKAVVKRI 216
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 147 IGPSSSVAIQVQLQLFNIPQIAYSATSMDSLSDKTLFKYFMRVVPDQAQARAVMDIV 206
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 217 QHF 219
:
:
:
207 KRY 209
:
:
:
RESULT 9
I49142
metabotropic glutamate receptor 8 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49142
R;Duvoisin, R.M.; Zhang, C.; Ramonell, K.
J. Neurosci. 15, 3075-3083, 1995
A>Title: A novel metabotropic glutamate receptor expressed in the retina and olfactory b
A:Reference number: I49142; MUID:95239344; PMID:7722646
A:Accession: I49142
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-308 <RES>
A:Cross-references: UNIPROT:P47743; EMBL:U17252; NID:9854728; PIDN:AAA68149.1; PID:g8547
C:Gene: mGluR8
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: neurotransmitter receptor
Query Match          19.8%; Score 225.5; DB 2; Length 908;
Best Local Similarity 28.6%; Pred. No. 6e-13;
Matches 59; Conservative 41; Mismatches 75; Indels 31; Gaps 5;
QY 20 FLWALGSEAKKEERTCRLLGKCVDAENHSLVIGGLFPIDS---RTIPANESILEP 76

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Db          21 FYWILTMQTHSQEVAHSIRLDG-----DIILGGLFFVHAKGSRGVPCGDLKKEKG 72
:
:
:
QY 77 SAKCEGFNFRFRWKKAMHMIKEINKRKDILPNITLGYQIFDTCFPTISKSEAVLVPLT 136
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 73 IHRLE-----AMLYAIDQTNKDPDLLNITLGVRLDTCSDRTVALEQSLTFVQ 121
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 137 GQ-EENRPNFRNSTGAPP-----AGIVGAGGSFLSPASRLGLYLPOVGYTSTCV 187
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 ALIEKADSDVKCANGDPPIFTKPKDKISGVIGAAASSVISINVANILRLFKIPQISYASTAP 181
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 188 IISDKYQPPSYLRVLTASDKIQSKAVV 213
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 ELSDNTRYDFFSRVPPDSYQAQAV 207
:
:
:
RESULT 10
A42916
metabotropic glutamate receptor mGluR5 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A42916
R;Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
J. Biol. Chem. 267, 13361-13368, 1992
A>Title: Molecular characterization of a novel metabotropic glutamate receptor mGluR5 co
A:Reference number: A42916; MUID:92317054; PMID:1320017
A:Accession: A42916
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1171 <ABE>
A:Cross-references: UNIPROT:P31424; GB:D10891; NID:9220813; PIDN:BA01711.1; PID:d100218
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBIN:107749, NCBI:107750)
C:Keywords: G protein-coupled receptor; transmembrane protein
Query Match          19.7%; Score 224.5; DB 2; Length 1171;
Best Local Similarity 30.2%; Pred. No. 1e-12;
Matches 55; Conservative 42; Mismatches 62; Indels 23; Gaps 6;
QY 53 LVIGGLFPIDRTIPANESILEPASAKC-----EGFNQFRFRWKKAMHMIKEINKRKDIL 108
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 35 IIGALFVSHQ--PTVDKVHE---RKGAVREQYGIQR---VEAMLHTLERINSDPTLL 86
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 109 PNITLGYQIFDTCF-----TISKSEAVLVLTGQENRPNFRNSTGAPP-----AGIV 157
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 87 PNITLGCIRDSCHWSAVALRQSEIFRDSLSISEEGLVRCVDSGSSFRSKKPIVGV 146
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 158 GAGGSFLSPASRLGLYLPOVGYTSTCVILSDKYQPPSYLRVLTASDKIQSKAVVKRI 217
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 147 GPGSSSVAIQVQLQLFNIPQIAYSATSMDSLSDKTLFKYFMRVVPDQAQARAVMDIV 206
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 218 HF 219
:
:
:
207 RY 208
:
:
:
RESULT 11
JH0563
metabotropic glutamate receptor 4 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: JH0563; I58149
R;Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A>Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002; PMID:1309649
A:Accession: JH0563
A:Molecule type: mRNA
A:Residues: 1-912 <TAN>
A:Cross-references: UNIPROT:P31423
A:Experimental source: brain
R;O'Hara, P.J.; Sheppard, P.O.; Thøgersen, H.; Venezia, D.; Haldeman, B.A.; McGrane, V.;
Neuron 11, 41-52, 1993

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A;Title: The ligand-binding domain in metabotropic glutamate receptors is related to bac  
A;Reference number: I58149; MUID:93332699; PMID:8338667  
A;Accession: J58149  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-123, 'R', 125-912 <RES>  
A;Cross-references: GB:M90518; NID:G205400; PIDN:AAA93190.1; PID:G205401  
C;Comment: This protein is coupled to a G protein and evokes a variety of functions by m  
C;Genetics:  
A;Gene: GLUR4  
C;Superfamily: metabotropic glutamate receptor 4  
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosph  
P;1-32/Domain: signal sequence #status predicted <SIG>  
F;33-912/Product: metabotropic glutamate receptor 4 #status predicted <MET>  
F;588-610/Domain: transmembrane #status predicted <TRI>  
F;625-645/Domain: transmembrane #status predicted <TRI>  
F;657-675/Domain: transmembrane #status predicted <III>  
F;700-720/Domain: transmembrane #status predicted <III>  
F;751-772/Domain: transmembrane #status predicted <TRV>  
F;786-807/Domain: transmembrane #status predicted <TRV>  
F;822-847/Domain: transmembrane #status predicted <VII>  
F;98,301,454,484,569/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;621,689,695,859,870/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 19.6%; Score 222.5; DB 2; Length 912;  
Best Local Similarity 32.9%; Pred. No. 1.1e-12;  
Matches 56; Conservative 34; Mismatches 63; Indels 17; Gaps 4;

QY 53 LVIGLFPIDSRTPANESILEPASAKCEGFNFQRFRRWKAMIMIKKIDILPNI 112  
Db ITLGLFPVHGR---GSEGKACGLKKEGIIH-----RLEAMLPALDRINDDPLLPNI 100

QY 113 LGYQIFDTCPTISKSVEAVLVLTGQ--EENRPNFRNSTGAPP-----AGIVGAGGSF 163  
Db LGARILDTCSRDTALQSLTFVQALIEKDTGTEVRCGSGGPPITKPERVVGIVGAGSS 160

QY 164 LSPVPSRILGLYLPQVGYTSTCVILSDKYQFSPVSLRVIASDKIQSKAVV 213  
Db VSIWVANILRLFKIPQISYASTAPDLSDNSRYDFSRVPSDTYQQAAMV 210

RESULT 12

JH0562  
metabotropic glutamate receptor 3 precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C;Accession: JH0562  
R;Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.  
Neuron 8, 169-179, 1992

A;Title: A family of metabotropic glutamate receptors.  
A;Reference number: JH0561; MUID:92110002; PMID:1309649  
A;Accession: JH0562  
A;Molecule type: mRNA  
A;Residues: 1-879 <TRAN>  
A;Cross-references: UNIPROT:P31422  
A;Experimental source: brain  
C;Comment: This protein is coupled to a G protein and evokes a variety of functions by m  
C;Superfamily: metabotropic glutamate receptor 4  
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane pro  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;23-879/Product: metabotropic glutamate receptor 3 #status predicted <MET>  
F;577-599/Domain: transmembrane #status predicted <TRI>  
F;614-634/Domain: transmembrane #status predicted <TRI>  
F;646-664/Domain: transmembrane #status predicted <III>  
F;689-709/Domain: transmembrane #status predicted <III>  
F;735-756/Domain: transmembrane #status predicted <TRV>  
F;770-791/Domain: transmembrane #status predicted <TRV>  
F;804-828/Domain: transmembrane #status predicted <VII>  
F;209,292,414,439/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;610,845/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 19.5%; Score 221.5; DB 2; Length 879;  
Best Local Similarity 30.9%; Pred. No. 1.4e-12;

Matches 56; Conservative 35; Mismatches 65; Indels 25; Gaps 5;

QY 53 LVIGLFPIDSRTPANESILEPASAKCEGFNFQRFRRWKAMIMIKKIDILPNI 111  
Db LVIGLFPINERKGTGTEB-----CGRINEDRGIQRLKMLPAIDELKNDYLLPGV 89

QY 112 TLGYQIFDTC-----FTISKSVEAVLVLTGQENRPNFRNSTGAPP-----AGIVG 158  
Db KLGVHLDTCSRDTVALEQSLBFVRASLTQVDS--AEYMCPCDGSYAIOENIPLIAGVIG 147

QY 159 AGGSFSLVSPASRILGLYLPQVGYTSTCVILSDKYQFSPVSLRVIASDKIQSKAVVRIQH 218  
Db GSYSSVSIOVANLLRFLQIPQISYASTSAKLSKSRIDYFARTVPPDFYQAKAWASILRF 207

QY 219 F 219  
Db 208 F 208

RESULT 13

A49874  
metabotropic glutamate receptor 7 - rat  
N;Alternate names: metabotropic glutamate receptor mGluR7  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: A49874; I57954  
R;Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; Nakanishi, J. Biol. Chem. 269, 1231-1236, 1994  
A;Title: Molecular characterization of a new metabotropic glutamate receptor mGluR7 cou  
A;Reference number: A49874; MUID:94117433; PMID:8288585  
A;Accession: A49874  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-915 <RES>  
A;Cross-references: UNIPROT:P35400; GB:D16817; NID:G458728; PIDN:BA04092.1; PID:G45872  
R;Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L.  
Mol. Pharmacol. 45, 367-372, 1994  
A;Title: Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric aci  
A;Reference number: I57954; MUID:94195260; PMID:8145723  
A;Accession: I57954  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-915 <RES>  
A;Cross-references: EMBL:U06832; NID:G459657; PIDN:AAA20655.1; PID:G459658  
C;Genetics:  
A;Gene: mGluR7  
C;Superfamily: metabotropic glutamate receptor 4  
C;Keywords: neurotransmitter receptor

Query Match 19.4%; Score 220.5; DB 2; Length 915;  
Best Local Similarity 29.2%; Pred. No. 1.8e-12;  
Matches 50; Conservative 41; Mismatches 61; Indels 19; Gaps 4;

QY 53 LVIGLFPIDSRTPANESILEPASAKCEGFNFQRFRRWKAMIMIKKIDILPNI 111  
Db VTLGLFPVHAK-----GPSGVPCGDIKRENGIHLKLEAMLVALDQINSPLLPNV 99

QY 112 TLGYQIFDTCPTISKSVEAVLVLTGQ--EENRPNFRNSTGAPP-----AGIVGAGGS 162  
Db TLGARILDTCSRDTVALEQSLTFVQALIQKTSVRCNTGBPPVFKVPEKVVGVIGAGSS 159

QY 163 FLSPVPSRILGLYLPQVGYTSTCVILSDKYQFSPVSLRVIASDKIQSKAVV 213  
Db SVSIWVANILRLFKIPQISYASTAPDLSDRYDFSRVVPDPDSFQAQAMV 210

RESULT 14

JC7683  
taste receptor Tir3 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: JC7683  
R;Kitagawa, M.; Kusakabe, Y.; Miura, H.; Ninomiya, Y.; Hino, A.

